
A New FACS Approach Isolates hESC Derived Endoderm Using Transcription Factors.

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Public Summary:

Gene expression profiles were obtained following FACS sorting of cells using combinations of transcription factors. We use this transcription factor FACS (tfFACS) methodology to perform a genomic analysis of hESC-derived endodermal lineages marked by combinations of SOX17, GATA4, and CXCR4, and find that triple positive cells have a much stronger definitive endoderm signature than other combinations of these markers. Additionally, SOX17(+) GATA4(+) cells can be obtained at a much earlier stage of differentiation, prior to expression of CXCR4(+) cells, providing an important new tool to isolate this earlier definitive endoderm subtype. Overall, tfFACS represents an advancement in FACS technology which broadly crosses multiple disciplines, most notably in regenerative medicine to redefine cellular populations.

Scientific Abstract:

We show that high quality microarray gene expression profiles can be obtained following FACS sorting of cells using combinations of transcription factors. We use this transcription factor FACS (tfFACS) methodology to perform a genomic analysis of hESC-derived endodermal lineages marked by combinations of SOX17, GATA4, and CXCR4, and find that triple positive cells have a much stronger definitive endoderm signature than other combinations of these markers. Additionally, SOX17(+) GATA4(+) cells can be obtained at a much earlier stage of differentiation, prior to expression of CXCR4(+) cells, providing an important new tool to isolate this earlier definitive endoderm subtype. Overall, tfFACS represents an advancement in FACS technology which broadly crosses multiple disciplines, most notably in regenerative medicine to redefine cellular populations.

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